

[illegible]

**B**

The figure displays three schematic diagrams of protein structures, labeled Gab1, Gab3, and Gab2. Each diagram represents a linear sequence of amino acids, with specific domains and motifs highlighted. A scale bar indicating 50 aa is provided at the top right.

- Gab1 (695 aa):** The structure starts with a black-shaded **PH domain**. Following this, there are several tyrosine (Y) residues, a proline (P) residue, a white-shaded box, another P residue, a third white-shaded box, a fourth P residue, a fifth white-shaded box, a sixth P residue, and a seventh white-shaded box. The sequence ends with a Y residue.
- Gab3 (595 aa):** The structure begins with a black-shaded **PH domain**. It is followed by a Y residue, a white-shaded box, another Y residue, a third white-shaded box, a fourth white-shaded box, a fifth white-shaded box, a sixth white-shaded box, a seventh white-shaded box, an eighth white-shaded box, and a ninth white-shaded box. The sequence ends with a Y residue.
- Gab2 (666 aa):** The structure starts with a black-shaded **PH domain**. It is followed by a Y residue, a white-shaded box, another Y residue, a third white-shaded box, a fourth white-shaded box, a fifth white-shaded box, a sixth white-shaded box, a seventh white-shaded box, an eighth white-shaded box, a ninth white-shaded box, a tenth white-shaded box, and an eleventh white-shaded box. The sequence ends with a Y residue.

C

Gab3	MSTG--D-TVCMGWLIKSPPERKLQRYAWRKRWFVLRGR	37
Gab2	MSGGGGDDVVCTGWLKSPPEKKLRRYAWKKRWFILRSGR	40
Gab1	MSGG--E-VVCSGWLKSPPEKKLKRYAWKRRWFVLRSGR	37
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Gab3	MSGNPDVLEYYRNKHSNKPIRVIDLSECTVWKHAGPGFIR	77
Gab2	MSGDPDVLEYYKNEHSKKPLRIINLNLCEQVD-AGLTFNK	79
Gab1	LTGDPDVLEYYKNDHAKKPIRIIDLNLCCQVD-AGLTFNK	76
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Gab3	KEFQKNFVFIVKTTSRTFYLVAKTEEEMQVWVHSISQVCN	117
Gab2	KELQDSFVFDIKTSERTFYLVAETEAMNKKWVQSICQICG	119
Gab1	KEFENSYIFDINTIDRIFYLVADSEEDMNKWVRCICDICG	116
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Figure 1B and C